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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/600,070	06/20/2003	Katherine W. Osteryoung	MSU-08153	5938
23535 MEDLEN & CA	7590 01/27/200 ARROLL, LLP	EXAMINER		
101 HOWARD SUITE 350		KUBELIK, ANNE R		
SAN FRANCIS	SCO, CA 94105		ART UNIT	PAPER NUMBER
			1638	
			MAIL DATE	DELIVERY MODE
			01/27/2009	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary		Applic	ation No.	Applicant(s)	Applicant(s)			
		10/60	0,070	OSTERYOUNG ET AL.				
		Exami	ner	Art Unit				
		Anne I	R. Kubelik	1638				
The MAILING DATE of this communication appears on the cover sheet with the correspondence address Period for Reply								
A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION. - Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication. - Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).								
Status								
2a)⊠ Thi 3)⊡ Sin	sponsive to communication(s) file is action is FINAL . Ice this application is in condition sed in accordance with the pract	2b)∏ This action for allowance exc	is non-final. ept for formal ma	·	e merits is			
Disposition	of Claims							
4a) 5)⊠ Cla 6)⊠ Cla 7)□ Cla 8)□ Cla		re withdrawn from						
 9) The specification is objected to by the Examiner. 10) The drawing(s) filed on is/are: a) accepted or b) objected to by the Examiner. Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a). Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d). 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152. 								
Priority und	er 35 U.S.C. § 119							
 12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f). a) All b) Some * c) None of: 1. Certified copies of the priority documents have been received. 2. Certified copies of the priority documents have been received in Application No 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)). * See the attached detailed Office action for a list of the certified copies not received. 								
2) Notice of 3) Informatic	References Cited (PTO-892) Draftsperson's Patent Drawing Review (I on Disclosure Statement(s) (PTO/SB/08) (s)/Mail Date	PTO-948)	Paper No	v Summary (PTO-413) o(s)/Mail Date if Informal Patent Application 				

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DETAILED ACTION

1. Claims 23-55 are pending. Claims 35-42 are withdrawn from consideration as being drawn to a nonelected invention.

2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claim Rejections - 35 USC § 112

3. Claims 43-55 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Neither the instant specification nor the originally filed claims appear to provide support for the sequence between the 420 amino acid long sequence and the 110 amino acid long sequence being of any size. The specification indicates that it is about 200 amino acids long (pg 15, lines 15-17).

Thus, such a recitation constitutes NEW MATTER. In response to this rejection, Applicant is required to point to support for the recitation or to cancel the new matter.

In the response filed 27 May 2008 Applicant urges that support if found on pg 15 (response pg 6).

This is not found persuasive for the reasons indicated above..

4. Claims 43-55 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described

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in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Due to Applicant's amendment of the claims, the rejection is different from the rejection set forth in the Office action mailed 26 February 2008, as applied to claims 23-26. Applicant's arguments filed 27 May 2008 have been fully considered but they are not persuasive.

The claims require a nucleic acid encoding a protein with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences, wherein decreasing the amount of the protein in a cell results in incomplete or no division in the cell or the cell's plastid.

The specification calls SEQ ID NO:2 FTN2 and describes its function as a protein that when its levels are decreased leads to incomplete or no division of a prokaryote or plastid, resulting in long filamentous cells in cyanobacteria and single or few very large chloroplasts in plants (pg 15, lines 1-10).

The specification describes Ftn2 proteins as having a DnaJ-like domain at its N-terminal half, but that this domain is missing the essential central HPD motif (pg 60, lines 7-10; pg 90, lines 12-17). Other motifs are described (pg 60, lines 11-20; pg 90, lines 17-27; Table 7), but such motifs are not present in every protein indicated to be an Ftn2 homolog.

The specification describes eight sequences, six from four bacteria species and two from plants, that as Ftn2 sequences. However neither of the plant sequences, SEQ ID NO:2 from Arabidopsis, nor the sequence from rice, SEQ ID NO:125, fall within the scope of the claims

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because SEQ ID NO:2 has 100% identity to SEQ ID NO:2 and the rice sequence has more than 6-20% identity to the middle portion of SEQ ID NO:2 (see below):

```
; Sequence 125, Application US/10600070; Publication No. US20040139500A1
; GENERAL INFORMATION:
  APPLICANT: Osteryoung, Katherine W.
  APPLICANT: Vitha, Stanislav
   APPLICANT: Koksharova, Olga A.
  APPLICANT: Gao, Hongo
TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of
   TITLE OF INVENTION: Use
   FILE REFERENCE: MSU-08153
   CURRENT APPLICATION NUMBER: US/10/600,070
  CURRENT FILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 206
   SOFTWARE: PatentIn version 3.2
 SEQ ID NO 125
LENGTH: 760
   TYPE: PRT
    ORGANISM: Oryza sativa
US-10-600-070-125
 Query Match 43.7%; Score 1775.5; DB 4; Length 760; Best Local Similarity 47.9%; Pred. No. 8.5e-140; Matches 390; Conservative 119; Mismatches 213; Indels 93; Gaps
          12 SPFQLCRLPPATTKLRRSHNTSTTIC-SASKWADRLLSDFNF----TSDSSSSSFATAT 65
Qy
                                 : | :||:||:|| :||:
          14 APFAFSLPRPRPRPRPRPPHPSAACRAASRWAERLFADFHLLPTAAPSDPPSPAPAPAA 73
Db
          66 TTATLVSLPPSIDRPERHVPIPIDFYQVLGAQTHFLTDGIRRAFEARVSKPPQFGFSDDA 125
                          74 APSASPFVPLFPDAAERSLPLQVDFYKVLGAEPHFLGDGIRRAFEARIAKPPQYGYSTDA 133
Db
         126 \ {\tt LISRRQILQAACETLSNPRSRREYNEGLLDDEEATVITDVPWDKVPGALCVLQEGGETEI} \ 185
Qу
             1: |||:|| | :|| | | || :|: | :: | : |: ||
         134 LVGRRQMLQIAHDTLMNQNSRTQYDRALSENREEALTMDIAWDK------EAGEALA 184
Db
         186 VLRVGEALLKERLPKSFKQDVVLVMALAFLDVSRDAMALDPPDFITGYEFVEEALKLLQE 245
Qy
         Db
         Qy
         245 DGASNLAPDLLSQIDETLEEITPRCVLELLSLPIDTEHHKKRQEGLQGARNILWSVGRGG 304
Db
Qу
         306 ASALVGGLTREKFMNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALALVAQAFIGKK 365
              305 IATVGGGFSREAFMNEAFLRMTSIEQMDFFSKTPNSIPPEWFEIYNVALAHVAQAIISKR 364
         366 PHLLQDADKQFQQLQQAKVMAMEIPAMLYDTRNNWEIDFGLERGLCALLIGKVDECRMWL 425
         365 PQFIMMADDLFEQLQKFNIGS----HYAYDN----EMDLALERAFCSLLVGDVSKCRMWL 416
Db
         \tt 426~GLDSEDSQYRNPAIVEFVLENSN-RDDNDDLPGLCKLLETWLAGVVFPRFRDTKDKKFKL~484
             417 GIDNESSPYRDPKILEFIVTNSSISEENDLLPGLCKLLETWLIFEVFPRSRDTRGMQFRL 476
Db
         485 GDYYDDPMVLSYLERVEVVQGSPLAAAATMARIGAE-----HVKASAMQALQKVFP-SR 537
Qy
             | ||||| :|::||:
                                                    ||::|:|| |||
         477 GDYYDDPEVLSYLERMEGGGASHLAAAAAIAKLGAQATAALGTVKSNAIQAFNKVFPLIE 536
Db
         538 YTDRNSAEPKDVQETVFSVDPVGNNVGRDGEPGVFIAEAVRPSENFETNDYAIRAGVSES 597
Qy
         537 QLDRSAMENT------ 559
Db
         598 SVDETTVEMSVADMLKEASVKILAAGVAIGLISLFSQKYFLKSSSSFQRKDMVSSMESD- 656
Qy
                          : |::||::||
         560 -----ENAPAHDSRNAALKIISAGALFALLAVIGAKY------LPRKRPLSAIRSEH 605
Db
         657 --VATIGSVRADDSEAL-----PRMDARTAENIVSKWQKIKSLAFGPDHRIEMLPEVL 707
Ov
                                   606 GSVAVANSVDSTDDPALDEDPVHIPRMDAKLAEDIVRKWQSIKSKALGPEHSVASLQEVL 665
Db
         708 DGRMLKIWTDRAAETAQLGLVYDYTLLKLSVDSVTVSADGTRALVEATLEESACLSDLVH 767
Qу
             666 DGNMLKVWTDRAAEIERHGWFWEYTLSDVTIDSITISLDGRRATVEATIDEAGQLTDVTE 725
```

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Not all proteins with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences have the same function as SEQ ID NO:2. An sequence from Arabidopsis, At3g19180, that falls with this structural description (See below), does not have the same function as FTN2, as it cannot complement FTN2 function in Arabidopsis (Vitha et al, 2003, Plant Cell 15:1918-1933; see pg 1927, right column, paragraph 2).

```
O8VY16 ARATH
    Q8VY16 ARATH
                    PRELIMINARY; PRT; 819 AA.
     01-MAR-2002, integrated into UniProtKB/TrEMBL.
     01-MAR-2002, sequence version 1.
     07-FEB-2006, entry version 10.
    Hypothetical protein At3g19180.
     Name=At3q19180;
     Arabidopsis thaliana (Mouse-ear cress).
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
     rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX
     NCBI_TaxID=3702;
     NUCLEOTIDE SEQUENCE.
     Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
     Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
    Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
     Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
     Distributed under the Creative Commons Attribution-NoDerivs License
     EMBL; AY074283; AAL66980.1; -; mRNA.
     Hypothetical protein.
    SEQUENCE 819 AA; 90751 MW; 6720083F4864657E CRC64;
                          10.6%; Score 431; DB 2; Length 819;
  Best Local Similarity 23.5%; Pred. No. 2.9e-18;
  Matches 200; Conservative 116; Mismatches 311; Indels 224; Gaps 32;
           56 SSSSSFATATTTATLVSLPPSIDRPERHVPIPIDFYQVLGAQTHFLTDGIRRAFEARVSK 115
Qу
           116 PPQFGFSDDALISRRQILQAACETLSNPRSRREYNEGLLDDEEATVITDVPWDKVPGALC 175
Qy
          125 DAEEGYTMEAAAARQDLLMDVRDKL---LFESEYAGNLKEKIAPKSPLRIPWAWLPGALC 181
          176 VLQEGGETEIVLRVGEALLKERLPKSFKQDVVLVMALAFLDVSRDAMALDPPDFITGYEF 235
          182 LLQEVGQEKLVLDIGRAALRNLDSKPYIHDIFLSMALAECAIAKAAFEVNKVS--QGFEA 239
          {\tt 236\ VEEALKLLQEE-GASSLAPDLRAQIDETLEEITPRYVLELLGLPLGDDYAAKRLNGLSGV\ 294}
Qу
                               11 | | | | | | | | | |
          240 LARAQSFLKSKVTLGKLA--LLTQIEESLEGLAPPCTLDLLGLPRTPENAERRGAIAAL 297
Db
          295 RNILWSVGGGGASALVGGLTREK-----FMNEAFLRMTAAEQVDLF-----VATP 339
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```
| :| | ||: | |:::| |: | ||| : 298 RELLRQ------GLSVEASCQIQDWPCFLSQAISRLLATEIVDLLPWDDLAITRK 346
Db
       Qy
       Db
       391 AMLYDTRNNWEIDFGLERGLCALLIGKVDECRMWLGL----DSEDSQYRNPAIVEFVLEN 446
Qv
       | : :| | |: : | | : || : || 397 A-----SEGVDLKFEEAFCSFLLKQGSEAEALEKLKQLESNSDSAVRNS-----ILGK 444
Db
       447 SNRDDNDDLPGLCKLLETWLAGVVFPRFRDTK------DKKFKLGDYYDDPMVL 494
Qy
       445 ESRSTS----ATPSLEAWLMESVLANFPDTRGCSPSLANFFRAEKKYPENKKMGSPSIM 499
       495 SY----LERVEVVQGSPLAAAATMARIGAEHVKASAMQALQKVFPSRYTDRNSAEPKD 548
Qу
       500 NHKTNQRPLSTTQFVNSS------QHL------YTAVEQLTPTD 531
Db
       549\ \text{VQETVFSVDPVGNNVGRDGEPGVFIAEAVRPSENFETNDYAIRAGVSESSV-DETTVEMS}\ 607
       Db
       636 VADMLKEASVKILAAGVAIGLISLFSQKY----- 636
Qу
       ::: || | :| || 572 QSSLIGRVSVVAL----LGCTVFFSLKLSGIRSGRLQSMPISVSARPHSESDSFLWKTE 626
Db
       637 ---FLKSSSSFQRKDMVSS------673
Qу
       Db
       674 -MDARTAENIVSKWQKIKSLAFGPDHRIEMLPEVLDGRMLKIWTDRAAETAQLGLVY-DY 731
Qy
       Db
       732 TLLKLSVDSVTVSAD---GTRALVEATLEESACLSDLVHPENNATDVRTYTTRYEVFWSK 788
Qy
                  : | | : | | | : | |
       746 VLLHLEVLQAHIFEDGIAGEAAEIEALLEEAAELVDESQPK-NAKYYSTYKIRYILKKQE 804
       789 SG-WKITEGSV 798
Qу
       805 DGLWKFCQSDI 815
```

The specification does not describe the structural features that distinguish plastid and prokaryotic cell division proteins with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences have the same function as SEQ ID NO:2 from other proteins with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences have the same function as SEQ ID NO:2.

The species described in the specification do not describe a representative number of species within the scope of this very large genus.

Therefore, one of skill in the art would not recognize that Applicant was in possession of the necessary common attributes or features of the genus in view of the disclosed species.

Because the nucleic acids are not described, cells transformed with a vector comprising them are likewise not described, and the specification fails to provide an adequate written description of the claimed invention.

Therefore, given the lack of written description in the specification with regard to the structural and functional characteristics of the compositions used in the claimed methods, Applicant does not appear to have been in possession of the claimed genus at the time this application was filed.

Applicant urges Fig 3B shows a functional and conserved domain (response pg 13-14).

This is not found persuasive because no such domain is shown in Fig 3B. Further, the specification does not describe the features that distinguish proteins that have Ftn2 function from those that do not.

Applicant urges a DnaJ domain is taught (response pg 14).

This is not found persuasive because more than a DnaJ-like domain is required for function.

Applicant urges sequences from 12 species are described (response pg 14-16).

This is not found persuasive because the sequences for a number of these do not appear to be in the specification, and the version of the other sequences available at the time of filing is not known. Further, one of these sequences is indicated to be a fragment.

5. Claims 43-55 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with

the enablement requirement. The claims contain subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Due to Applicant's amendment of the claims, the rejection is different from the scope of enablement rejection set forth in the Office action mailed 26 February 2008, as applied to claims 23-34. Applicant's arguments filed 27 May 2008 have been fully considered but they are not persuasive.

The claims are broadly drawn to cells transformed with a vector comprising a nucleic acid encoding a protein with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences, wherein decreasing the amount of the protein in a cell results in incomplete or no division in the cell or the cell's plastid.

The instant specification describes the isolation of Ftn2 from *Synechococcus* and identification of putative cyanobacterial homologs (examples 4 and 5), which has 17% identity to an unknown protein (SEQ ID NO:2, encoded by the genomic sequence SEQ ID NO:3 and cDNA SEQ ID NO:1) in *Arabidopsis*; mapping the *arc6* mutation in *Arabidopsis* to show that it and the unknown protein map to chromosome 5 (example 2); rescuing the *arc6* mutation by SEQ ID NO:1 (example 2); analysis of the mutant to show that FtsZ rings and filaments are disrupted (example 2); identification of potential Ftn2 homologues from various database sequences (example 3); isolation of an Ftn2 gene from Synechococcus by transposon mutagenesis (examples 4-5); identification of arc5 (examples 6) and Fzo-like (example 7) genes from *Arabidopsis*. The specification teaches that SEQ ID NO:2 does not have a proper DnaJ domain or a complete myb domain, but appears to have a chloroplast targeting sequence and three

putative transmembrane helices (pg 90-91).

The invention would not function as claimed

The claims are drawn to cells transformed with a vector comprising a nucleic acid encoding a protein, wherein decreasing the amount of the protein in a cell results in incomplete or no division in the cell or the cell's plastid. Thus, the claims are drawn to cells transformed with a vector in which decreasing the expression of the product produced by the vector produces a new phenotype.

However, cells transformed with a vector that do not produce the product encoded by the vector would be equivalent to cells that are not transformed with the nucleic acid, that is, they would be phenotypically wild-type.

There is no reason that such cells would have incomplete or no division. Therefore, these cells are not enabled.

The specification does not teach nucleic acids within the full scope of the claims

Not all proteins with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences have the same function as SEQ ID NO:2. An sequence from Arabidopsis, At3g19180, that falls with this structural description (See sequence comparison in the written description rejection above), does not have the same function as FTN2, as it cannot complement FTN2 function in Arabidopsis (Vitha et al, 2003, Plant Cell 15:1918-1933; see pg 1927, right column, paragraph 2).

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The specification does not teach how to make functional nucleic acids encoding a protein with 20-60% identity to 420 amino acids at the N-terminus of SEQ ID NO:2, 15-55% identity to an 100 amino acid sequence at the C-terminus of SEQ ID NO:2 and 6-20% identity to the region between those two sequences, wherein decreasing the amount of the protein in a cell results in incomplete or no division in the cell or the cell's plastid.

Additionally, even 5 years after the filing of the instant application, the function of Ftn2 is not known (Maple et al, 2007, Annals Botany 99:565-579; pg 570, right column, paragraph 2).

Also, Arc6 (the instant SEQ ID NO:2) appears to have a very different function in plants than

Ftn2 does in prokaryotes (pg 570, right column, paragraph, to pg 571, right column, paragraph 2).

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled.

Applicant urges the specification teaches how to use the claimed nucleic acids to increase or decrease plastid size and shape (response pg 9).

This is not found persuasive because although the specification does not teach how to use plants in which Ftn2 is overexpressed, Vitha et al (2003, Plant Cell 15:1918-1933) teach that such plants have the same phenotype as plants in which the expression of SEQ ID NO:2 is depressed (pg 1923, right column, paragraph 2); thus, this portion of the previous rejection is withdrawn.

6. Claims 23-34 are allowed.

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Conclusion

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7. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, Ph.D., whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg, can be reached at (571) 272-0975.

The central fax number for official correspondence is (571) 273-8300.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

January 27, 2009

/Anne R. Kubelik/ Primary Examiner, Art Unit 1638